

OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:57:24 ; Search time 4550.28 Seconds
(without alignments)
9527.774 Million cell updates/sec

Title: US-10-670-863-2_COPY_213_1274
Perfect score: 1062
Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

- 1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
- 14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
- 15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
- 16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
- 17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
- 18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
- 19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
- 20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
- 21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
- 22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
- 23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
- 24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
- 25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
- 26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
- 27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
- 28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
- 29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
- 30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
- 31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
- 32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
- 33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
- 34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
- 35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
- 36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
- 37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
- 38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*

39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq: *
40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq: *
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42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq: *
43: /cgn2_6/ptodata/1/pna/US099E_COMB.seq: *
44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq: *
45: /cgn2_6/ptodata/1/pna/US099G_COMB.seq: *
46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq: *
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48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq: *
49: /cgn2_6/ptodata/1/pna/US101B_COMB.seq: *
50: /cgn2_6/ptodata/1/pna/US102A_COMB.seq: *
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52: /cgn2_6/ptodata/1/pna/US103A_COMB.seq: *
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54: /cgn2_6/ptodata/1/pna/US104A_COMB.seq: *
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56: /cgn2_6/ptodata/1/pna/US105A_COMB.seq: *
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59: /cgn2_6/ptodata/1/pna/US107A_COMB.seq: *
60: /cgn2_6/ptodata/1/pna/US107B_COMB.seq: *
61: /cgn2_6/ptodata/1/pna/US107C_COMB.seq: *
62: /cgn2_6/ptodata/1/pna/US107D_COMB.seq: *
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64: /cgn2_6/ptodata/1/pna/US108B_COMB.seq: *
65: /cgn2_6/ptodata/1/pna/US109A_COMB.seq: *
66: /cgn2_6/ptodata/1/pna/US109B_COMB.seq: *
67: /cgn2_6/ptodata/1/pna/US109C_COMB.seq: *
68: /cgn2_6/ptodata/1/pna/US110_COMB.seq: *
69: /cgn2_6/ptodata/1/pna/US6000_COMB.seq: *
70: /cgn2_6/ptodata/1/pna/US6001_COMB.seq: *
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72: /cgn2_6/ptodata/1/pna/US6003_COMB.seq: *
73: /cgn2_6/ptodata/1/pna/US6004_COMB.seq: *
74: /cgn2_6/ptodata/1/pna/US6005_COMB.seq: *
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78: /cgn2_6/ptodata/1/pna/US6009_COMB.seq: *
79: /cgn2_6/ptodata/1/pna/US6010_COMB.seq: *
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88: /cgn2_6/ptodata/1/pna/US6019_COMB.seq: *
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91: /cgn2_6/ptodata/1/pna/US6022_COMB.seq: *
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93: /cgn2_6/ptodata/1/pna/US6023B_COMB.seq: *
94: /cgn2_6/ptodata/1/pna/US6024_COMB.seq: *
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96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq: *
97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq: *
98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq: *
99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq: *
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101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq: *
102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq: *
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq: *
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq: *
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq: *

106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
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 108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:*
 109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
 110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
 111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*
 112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq:*
 113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:*
 114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:*
 115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq:*
 116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq:*
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 118: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:*
 119: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:*
 120: /cgn2_6/ptodata/1/pna/US6050_COMB.seq:*
 121: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
 122: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
 123: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
 124: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
 125: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
 126: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
 127: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
 128: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
 129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:38:19 ; Search time 1620.48 Seconds
 (without alignments)
 8309.150 Million cell updates/sec

Title: US-10-670-863-2_COPY_213_1274
 Perfect score: 1062
 Sequence: 1 atgacagcaaagcctctaag.....tccggttatgggttctgtaag 1062

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 21945288 seqs, 6339366203 residues

Total number of hits satisfying chosen parameters: 43890576

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_NA_New:*
 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
 2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
 3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
 7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
 8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
 9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq10:*
 10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
 11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
 12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*

13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq6:*
15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq7:*
16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq8:*
17: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq9:*
18: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
19: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
20: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
21: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq4:*
22: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq5:*
23: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:22:19 ; Search time 177.454 Seconds
(without alignments)
9183.943 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_1274
Perfect score: 996
Sequence: 1 acaccagaaatctcatgcag.....tccggttatgggttctgtaag 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 00:34:19 ; Search time 704.717 Seconds
(without alignments)
9161.687 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_1274
Perfect score: 996
Sequence: 1 acaccagaaatctcatgcag.....tccggttatgggttctgtaag 996

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 22:57:24 ; Search time 4267.5 Seconds
(without alignments)
9527.774 Million cell updates/sec

Title: US-10-670-863-2_COPY_279_i274

Perfect score: 996

Sequence: 1 acaccagaaatctcatgcag.....tccggttatgggttctgtaag 996

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_NA Main:*

```
1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US07_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US083_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/US084_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US085_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
14: /cgn2_6/ptodata/1/pna/US088_COMB.seq:*
15: /cgn2_6/ptodata/1/pna/US089_COMB.seq:*
16: /cgn2_6/ptodata/1/pna/US090_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US091_COMB.seq:*
18: /cgn2_6/ptodata/1/pna/US092A_COMB.seq:*
19: /cgn2_6/ptodata/1/pna/US092B_COMB.seq:*
20: /cgn2_6/ptodata/1/pna/US093A_COMB.seq:*
21: /cgn2_6/ptodata/1/pna/US093B_COMB.seq:*
22: /cgn2_6/ptodata/1/pna/US094_COMB.seq:*
23: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:*
24: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:*
25: /cgn2_6/ptodata/1/pna/US095C_COMB.seq:*
26: /cgn2_6/ptodata/1/pna/US095D_COMB.seq:*
27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:*
28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:*
29: /cgn2_6/ptodata/1/pna/US096C_COMB.seq:*
30: /cgn2_6/ptodata/1/pna/US096D_COMB.seq:*
31: /cgn2_6/ptodata/1/pna/US096E_COMB.seq:*
32: /cgn2_6/ptodata/1/pna/US097A_COMB.seq:*
33: /cgn2_6/ptodata/1/pna/US097B_COMB.seq:*
34: /cgn2_6/ptodata/1/pna/US097C_COMB.seq:*
35: /cgn2_6/ptodata/1/pna/US098A_COMB.seq:*
36: /cgn2_6/ptodata/1/pna/US098B_COMB.seq:*
37: /cgn2_6/ptodata/1/pna/US098C_COMB.seq:*
38: /cgn2_6/ptodata/1/pna/US098D_COMB.seq:*
39: /cgn2_6/ptodata/1/pna/US099A_COMB.seq:*
40: /cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
41: /cgn2_6/ptodata/1/pna/US099C_COMB.seq:*
42: /cgn2_6/ptodata/1/pna/US099D_COMB.seq:*
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44: /cgn2_6/ptodata/1/pna/US099F_COMB.seq:*
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46: /cgn2_6/ptodata/1/pna/US100A_COMB.seq:*
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48: /cgn2_6/ptodata/1/pna/US101A_COMB.seq:*
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Listing first 45 summaries

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Best Local Similarity 100.0%; Pred. No. 1.6e-205;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MTAKPLR ^T TVLSLLFFALSGVLGTPEI ^S CRNEYGEAVDWFIF ^Y KLPKRTSKASEEAGLQYL	60
Qy	61	YLDSTRQTWNKSLYLINSTRSALGRTLQHL ^Y DTHNSTNDTAYLI ^Y NDGVPGSVNYSRQYG	120
Db	61	YLDSTRQTWNKSLYLINSTRSALGRTLQHL ^Y DTHNSTNDTAYLI ^Y NDGVPGSVNYSRQYG	120
Qy	121	HAKGLLVWNRTQGF ^W L ^I HSVPKFPPVHG ^Y EYPTSGRRYQGTGICITFGYSQFEEIDFQLL	180
Db	121	HAKGLLVWNRTQGF ^W L ^I HSVPKFPPVHG ^Y EYPTSGRRYQGTGICITFGYSQFEEIDFQLL	180
Qy	181	VLQPN ^I YSCFIPSTFHWKLI ^Y MPRMCANSSSLKI ^P VR ^Y LAELHSAQGLN ^F VHFAKSSFYT	240
Db	181	VLQPN ^I YSCFIPSTFHWKLI ^Y MPRMCANSSSLKI ^P VR ^Y LAELHSAQGLN ^F VHFAKSSFYT	240
Qy	241	DDIFTGWIAQKLKTHLLAQT ^W QKKKQELPSNCSLPYHVYNI ^K SIGVTSKSYFSSRQDHSK	300
Db	241	DDIFTGWIAQKLKTHLLAQT ^W QKKKQELPSNCSLPYHVYNI ^K SIGVTSKSYFSSRQDHSK	300
Qy	301	WCVSIKGSANRWTCIGDLN ^R SLHQALRGGGFICTKNHYI ^Y QAFHKLYLRYGFCK	354
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; Sequence 1, Application US/09807784B
; Patent No. 6653118
; GENERAL INFORMATION:
; APPLICANT: Tanuma, Sei-ichi
; APPLICANT: Shiokawa, Daisuke
; TITLE OF INVENTION: No. 6653118e1 Deoxyribonuclease, Gene Encoding Thereof and Use Thereof
; FILE REFERENCE: 210792
; CURRENT APPLICATION NUMBER: US/09/807,784B
; CURRENT FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: JP 11-230870
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
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; SEQ ID NO 1
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-807-784B-1

Query Match 100.0%; Score 1927; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.6e-205;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MTAKPLRTVLSLLFFALSGVLGTPEISCRNEYGEAVDWFIFYKLPKRTSKASEEAGLQYL 60

Qy     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLVDTHNSTNDTAYLIYNDGVPGSVNYSRQYG 120
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Db     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLVDTHNSTNDTAYLIYNDGVPGSVNYSRQYG 120

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Db    121 HAKGLLVWNRQTQGFVLIHSPVKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL 180

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Qy    301 WCVSIKGSANRWTCIGDLNRSLSLHQAALRGGGFICTKNHYIYQAFHKLYLRYGFCK 354
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RESULT 3

US-09-949-434-2

; Sequence 2, Application US/09949434
; Patent No. 6767997
; GENERAL INFORMATION:
; APPLICANT: Eastman, Alan R.
; APPLICANT: Krieser, Ronald J.
; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS
; FILE REFERENCE: DC-0137
; CURRENT APPLICATION NUMBER: US/09/949,434
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 09/574,942
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Mus sp.

US-09-949-434-2

Query Match 100.0%; Score 1927; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.6e-205;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 YLDSTRQTNKSLYLYINSTRSALGRTLQHLVDTHNSTNDTAYLIYNDGVPGSVNYSRQYG 120
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Db	121	HAKGLLVWNR	TQGF	LIHS	VPKF	PPVH	GYEY	PTSG	RRYG	QTGI	CITF	GYSQ	FEEI	DFQL	180			
Qy	181	VLQPN	IYSC	FI	PSTF	HWKL	IYMP	RCAN	SSSL	KI	PVRY	LAE	LHSA	QGLN	FVHF	AKSS	FYT	240
Db	181	VLQPN	IYSC	FI	PSTF	HWKL	IYMP	RCAN	SSSL	KI	PVRY	LAE	LHSA	QGLN	FVHF	AKSS	FYT	240
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Db	241	DDIFT	GWIA	QKLK	THLL	AQTW	QKKK	QELP	SNCS	LPYH	VYNI	KSIG	VTSK	SYFS	SRQD	HSK	300	
Qy	301	WCVSI	KGSAN	RWTC	IGDL	NRSL	HQAL	RGGG	FICT	KNHY	IYQA	FKLY	LRYG	FCK	354			
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RESULT 2

US-09-541-840-2

; Sequence 2, Application US/09541840

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0125

; CURRENT APPLICATION NUMBER: US/09/541,840

; CURRENT FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-541-840-2

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Qy	61	YLDSTR	QTNK	SLYL	INSTR	SALGR	TLQH	LYDTH	NSTND	TAYLI	YNDG	VPGS	VNYS	RQYG	120			
Db	61	YLDSTR	QTNK	SLYL	INSTR	SALGR	TLQH	LYDTH	NSTND	TAYLI	YNDG	VPGS	VNYS	RQYG	120			
Qy	121	HAKGLLVWNR	TQGF	LIHS	VPKF	PPVH	GYEY	PTSG	RRYG	QTGI	CITF	GYSQ	FEEI	DFQL	180			
Db	121	HAKGLLVWNR	TQGF	LIHS	VPKF	PPVH	GYEY	PTSG	RRYG	QTGI	CITF	GYSQ	FEEI	DFQL	180			
Qy	181	VLQPN	IYSC	FI	PSTF	HWKL	IYMP	RCAN	SSSL	KI	PVRY	LAE	LHSA	QGLN	FVHF	AKSS	FYT	240
Db	181	VLQPN	IYSC	FI	PSTF	HWKL	IYMP	RCAN	SSSL	KI	PVRY	LAE	LHSA	QGLN	FVHF	AKSS	FYT	240
Qy	241	DDIFT	GWIA	QKLK	THLL	AQTW	QKKK	QELP	SNCS	LPYH	VYNI	KSIG	VTSK	SYFS	SRQD	HSK	300	
Db	241	DDIFT	GWIA	QKLK	THLL	AQTW	QKKK	QELP	SNCS	LPYH	VYNI	KSIG	VTSK	SYFS	SRQD	HSK	300	
Qy	301	WCVSI	KGSAN	RWTC	IGDL	NRSL	HQAL	RGGG	FICT	KNHY	IYQA	FKLY	LRYG	FCK	354			
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RESULT 2

US-09-541-840-2

; Sequence 2, Application US/09541840

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0125

; CURRENT APPLICATION NUMBER: US/09/541,840

; CURRENT FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-541-840-2

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 Best Local Similarity 100.0%; Pred. No. 4.3e-173;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MTAKPLRRTVLSLLFFALSGVLGTPEISCRNEYGEAVDWFIFYKLPKRTSKASEEAGLQYL	60
Qy	61	YLDSTRQTNKSLYLINSTRSALGRTLQHLYDTHNSTNDTAYLIYNDGVPGSVNYSRQYG	120
Db	61	YLDSTRQTNKSLYLINSTRSALGRTLQHLYDTHNSTNDTAYLIYNDGVPGSVNYSRQYG	120
Qy	121	HAKGLLVNRTQGFWLIHSVPKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL	180
Db	121	HAKGLLVNRTQGFWLIHSVPKFPPVHGYEYPTSGRRYGQTGICITFGYSQFEEIDFQLL	180
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Qy	301	ATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGACTAGCA	360
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Qy	361	AGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAACCTGGA	420
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Qy	481	TGTATGACACACATAAATTCACGAATGACACAGCCTATCTAATATACAACGATGGTGTCC	540
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Qy	541	CTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTATGGAACA	600
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Db	601	 GAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCCAGTTCATGGCTATG	660
Qy	661	AGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCGGATACA	720
Db	661	 AGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTCGGATACA	720
Qy	721	GCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACAGCTGCT	780
Db	721	 GCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACAGCTGCT	780
Qy	781	TCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCAACTCCA	840
Db	781	 TCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCAACTCCA	840
Qy	841	GTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTCTAAACT	900
Db	841	 GTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTCTAAACT	900
Qy	901	TCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGATAGCTC	960
Db	901	 TCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGATAGCTC	960
Qy	961	AAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGCTTCCTT	1020
Db	961	 AAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGCTTCCTT	1020
Qy	1021	CAAACTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTTCCAAGT	1080
Db	1021	 CAAACTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTTCCAAGT	1080
Qy	1081	CTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCTCCGCAA	1140
Db	1081	 CTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCTCCGCAA	1140
Qy	1141	ATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAGGTGGAG	1200
Db	1141	 ATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAGGTGGAG	1200
Qy	1201	GATTTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATCTCCGTT	1260
Db	1201	 GATTTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATCTCCGTT	1260

Qy	1261	ATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACACTGGCA	1320
Db	1261	ATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACACTGGCA	1320
Qy	1321	CTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAGCACAAC	1380
Db	1321	CTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAGCACAAC	1380
Qy	1381	GTAGCGTCCAATAAAAGCACTGTGAGCCACATTTACCTTCCTATGTTCAAATCAAGAGA	1440
Db	1381	GTAGCGTCCAATAAAAGCACTGTGAGCCACATTTACCTTCCTATGTTCAAATCAAGAGA	1440
Qy	1441	AATAGGAGTCATCTGCATGTATGGAATTAGAAATCAAAATCATGATATGTAAGTAATAGC	1500
Db	1441	AATAGGAGTCATCTGCATGTATGGAATTAGAAATCAAAATCATGATATGTAAGTAATAGC	1500
Qy	1501	ACCAGGGGACAGAATACAATATTTTCTCCAGTTTAATTACCTTCAGTGGTCTGTCTTGT	1560
Db	1501	ACCAGGGGACAGAATACAATATTTTCTCCAGTTTAATTACCTTCAGTGGTCTGTCTTGT	1560
Qy	1561	GGATTAAGTTTCATCTCTCACAAAGCAACCCTGACTGTCCTGTTTGAAGAAATAAAGGTG	1620
Db	1561	GGATTAAGTTTCATCTCTCACAAAGCAACCCTGACTGTCCTGTTTGAAGAAATAAAGGTG	1620
Qy	1621	CCCTCCTCCCCCTTAAAAAAAAAAAAAAAAAAAA	1652
Db	1621	CCCTCCTCCCCCTTAAAAAAAAAAAAAAAAAAAA	1652

RESULT 7

AF178974

LOCUS AF178974 1498 bp mRNA linear ROD 29-NOV-1999

DEFINITION Rattus norvegicus deoxyribonuclease DLAD mRNA, complete cds.

ACCESSION AF178974

VERSION AF178974.1 GI:6470130

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1498)

AUTHORS Tanuma,S. and Shiokawa,D.

TITLE Cloning of a cDNA encoding a rat DNase II-like acid DNase

JOURNAL Biochem. Biophys. Res. Commun. 265 (2), 395-399 (1999)

MEDLINE 20025354

PUBMED 10558878

REFERENCE 2 (bases 1 to 1498)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1999) Biochemistry, Science University of Tokyo,
Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

FEATURES

source Location/Qualifiers

1. .1498

/organism="Rattus norvegicus"

/mol_type="mRNA"

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159. .1229

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PRRTSRGGTGMGLDYLYLDS'TMRTWSKSHHLINSSRSSLGRTLEQLYEAHNAKNDTAY
LIYNDAVPASVNYSGNYGHAKGLLVWNRVQGFVLIHSIPKFPVPEKGYEYPSSGRQY
AQSGLCITLKYSQYETIDSQLLVFQPNIYSCFIPNIFRWELIHMPQMCAKSSASKIPS

ORIGIN

[illegible]

Qy	175	CACAGTCCCCTGTCATGGAATGAAGGCCACAGATAGAAAAATGACAGCAAAGCCTCTAAGAA	234
Db	2	CCCAGTCCCCTGTCATGGAATGAAGGCCACAGATAGAAAAATGACAGCAAAGCCTCTAAGAA	61
Qy	235	CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCTCTGGGGACACCAGAAATCTCAT	294
Db	62	CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCTCTGGGGACACCAGAAATCTCAT	121
Qy	295	GCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGA	354
Db	122	GCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGA	181
Qy	355	CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA	414
Db	182	CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA	241
Qy	415	CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC	474
Db	242	CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC	301
Qy	475	AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG	534
Db	302	AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG	361
Qy	535	GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT	594
Db	362	GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT	421
Qy	595	GGAACAGAACGCAGGGGTTCTGGCTGATACTCTGTTCCCAAGTTTCCCCAGTTCATG	654
Db	422	GGAACAGAACGCAGGGGTTCTGGCTGATACTCTGTTCCCAAGTTTCCCCAGTTCATG	481
Qy	655	GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG	714
Db	482	GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG	541
Qy	715	GATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACA	774
Db	542	GATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTGGTCTTACAACCAAACATCTACA	601
Qy	775	GCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCA	834
Db	602	GCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCA	661
Qy	835	ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC	894
Db	662	ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC	721
Qy	895	TAAACTTCGTCCATTTTGCAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA	954
Db	722	TAAACTTCGTCCATTTTGCAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA	781
Qy	955	TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC	1014
Db	782	TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC	841
Qy	1015	TTCCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT	1074
Db	842	TTCCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT	901
Qy	1075	CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT	1134
Db	902	CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT	961
Qy	1135	CCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG	1194

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Db      962 CCGCAAATCGCTGGACCTGCATTTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG 1021
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Db      1022 GTGGAGGATTTCATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAAATTATATC 1081
Qy      1255 TCCGTTTATGGGTTCTGTAAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCCTTGAAAACA 1314
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Db      1082 TCCGTTTATGGGTTCTGTAAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCCTTGAAAACA 1141
Qy      1315 CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAG 1374
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Db      1142 CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATATCAAGGCTTCTGAGTGAG 1201
Qy      1375 CACAACGTAGCGTCCAATAAAAAG 1397
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Db      1202 CACAACGTAGCGTCCAATAAAAAG 1224

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RESULT 3

US-09-949-434-1

; Sequence 1, Application US/09949434

; Patent No. 6767997

; GENERAL INFORMATION:

; APPLICANT: Eastman, Alan R.

; APPLICANT: Krieser, Ronald J.

; TITLE OF INVENTION: DEOXYRIBONUCLEASE II BETA PROTEINS AND cDNAS

; FILE REFERENCE: DC-0137

; CURRENT APPLICATION NUMBER: US/09/949,434

; CURRENT FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: 09/574,942

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1224

; TYPE: DNA

; ORGANISM: Mus sp.

US-09-949-434-1

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Query Match          73.8%;  Score 1219.8;  DB 4;  Length 1224;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 1221;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db      2   CCCAGTCCCCTGCATGGAATGAAGGCCACAGATAGAAAATGACAGCAAAGCCTCTAAGAA 61
Qy      235 CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCCTGGGGACACCAGAAATCTCAT 294
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      62  CAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTCCTGGGGACACCAGAAATCTCAT 121
Qy      295 GCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGA 354
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Db      122 GCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATCTTTTATAAGTTACCCAAAAGGA 181
Qy      355 CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA 414
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      182 CTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTGTACCTGGACTCCACAAGACAAA 241
Qy      415 CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC 474
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Db      242 CCTGGAACAAGAGCCTCTACCTGATTAACAGCACCAGGAGTGCTCTGGGGAGGACCTTAC 301
Qy      475 AGCATCTGTATGACACACATAATTCCACGAATGACACAGCCTATCTAATATACAACGATG 534
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Qy	535	GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT	594
Db	362	GTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGACATGCCAAAGGTCTGCTGGTAT	421
Qy	595	GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCCAGTTCATG	654
Db	422	GGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTTCCCAAGTTTCCCCCAGTTCATG	481
Qy	655	GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG	714
Db	482	GCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAAACCGGCATCTGCATCACTTTTCG	541
Qy	715	GATACAGCCAGTTTGTAGGAAATAGATTTTTCAGCTCTTGGTCTTACAACCAAACATCTACA	774
Db	542	GATACAGCCAGTTTGTAGGAAATAGATTTTTCAGCTCTTGGTCTTACAACCAAACATCTACA	601
Qy	775	GCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCA	834
Db	602	GCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATCTACATGCCCCGGATGTGTGCCA	661
Qy	835	ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC	894
Db	662	ACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCTGAACTGCACTCAGCCCAGGGTC	721
Qy	895	TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA	954
Db	722	TAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACTGATGACATCTTTACAGGATGGA	781
Qy	955	TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC	1014
Db	782	TAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACCTGGCAGAAAAAGAAACAAGAGC	841
Qy	1015	TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT	1074
Db	842	TTCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAACATCAAGTCCATTGGGGTAACTT	901
Qy	1075	CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT	1134
Db	902	CCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAATGGTGTGTTTCCATAAAGGGCT	961
Qy	1135	CCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG	1194
Db	962	CCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGAAGCCTACACCAAGCCTTAAGAG	1021
Qy	1195	GTGGAGGATTATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAATTATATC	1254
Db	1022	GTGGAGGATTATCTGTACAAAGAATCACTACATTTACCAGGCATTTTCATAAATTATATC	1081
Qy	1255	TCCGTTATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA	1314
Db	1082	TCCGTTATGGGTTCTGTAAGTAAACTCGGTGAAAGGCCACACCCTCTGTCCTTGAAAACA	1141
Qy	1315	CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATTTCAAGGCTTCTGAGTGAG	1374
Db	1142	CTGGCACTGGAACATCTCGCCTTGGATCTGTTCTCCATAATATCAAGGCTTCTGAGTGAG	1201
Qy	1375	CACAACGTAGCGTCCAATAAAAAG	1397
Db	1202	CACAACGTAGCGTCCAATAAAAAG	1224

RESULT 4

US-09-574-942-3

; Sequence 3, Application US/09574942

; Patent No. 6358723

; GENERAL INFORMATION:


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Location/Qualifiers
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/clone="IMAGE:1450676"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGACA."

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Query Match 32.9%; Score 543; DB 1; Length 543;
Best Local Similarity 100.0%; Pred. No. 4.9e-145;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Db

541 ACA 543

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Db	513		GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA	572
Qy	361		CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTCTGGCTGATACACTCTGTT	420
Db	573		CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTCTGGCTGATACACTCTGTT	632
Qy	421		CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA	480
Db	633		CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA	692
Qy	481		ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG	540
Db	693		ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG	752
Qy	541		GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	600
Db	753		GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	812
Qy	601		TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	660
Db	813		TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	872
Qy	661		GAAGTGCATCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	720
Db	873		GAAGTGCATCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	932
Qy	721		GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAACC	780
Db	933		GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAACC	992
Qy	781		TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	840
Db	993		TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	1052
Qy	841		ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAA	900
Db	1053		ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAA	1112
Qy	901		TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	960
Db	1113		TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	1172
Qy	961		AGCCTACACCAAGCCTTAAGAGGTGGAGGATTATCTGTACAAAGAATCACTACATTTAC	1020
Db	1173		AGCCTACACCAAGCCTTAAGAGGTGGAGGATTATCTGTACAAAGAATCACTACATTTAC	1232
Qy	1021		CAGGCATTTTCATAAAATTATATCTCCGTTATGGGTTCTGTAAG	1062
Db	1233		CAGGCATTTTCATAAAATTATATCTCCGTTATGGGTTCTGTAAG	1274

RESULT 7

AF178974

LOCUS AF178974 1498 bp mRNA linear ROD 29-NOV-1999

DEFINITION Rattus norvegicus deoxyribonuclease DLAD mRNA, complete cds.

ACCESSION AF178974

VERSION AF178974.1 GI:6470130

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 1498)

AUTHORS Tanuma,S. and Shiokawa,D.

TITLE Cloning of a cDNA encoding a rat DNase II-like acid DNase

JOURNAL Biochem. Biophys. Res. Commun. 265 (2), 395-399 (1999)

MEDLINE 20025354

PUBMED 10558878

REFERENCE 2 (bases 1 to 1498)

AUTHORS Shiokawa,D. and Tanuma,S.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1999) Biochemistry, Science University of Tokyo, Shinjuku-ku Ichigaya Funagawara-machi 12, Tokyo 162-0826, Japan

FEATURES

Location/Qualifiers

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CDS 159..1229

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/protein_id="AAF13596.1"

/db_xref="GI:6470131"

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CSKNRYIYQSFDRLVSHYASCN"

ORIGIN

Query Match 72.6%; Score 771.4; DB 10; Length 1498;

Best Local Similarity 83.4%; Pred. No. 3.9e-220;

Matches 890; Conservative 0; Mismatches 171; Indels 6; Gaps 1;

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Qy	61	CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC	120
Db	219	CTGGGGACACCAGTAATCTCGTGCATAAACGAAGATGGTAAAGCCGTGGACTGGTTTGCC	278
Qy	121	TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG	180
Db	279	TTTTATAAGTTACCCAGAAGGACCAGCAGAGGAGGTACAGGGATGGGGCTGGATTACCTG	338
Qy	181	TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAAACAGCACCAGG	240
Db	339	TACCTGGACTCCACAATGAGAACCTGGAGCAAGAGCCACCACCTGATTAAACAGCAGCAGG	398
Qy	241	AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA	300
Db	399	AGCTCCCTGGGAAGGACCTTGGAGCAGCTGTATGAAGCACACAATGCCAAGAATGACACA	458
Qy	301	GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA	360
Db	459	GCCTATCTGATATACAATGACGCTGTCCCTGCATCTGTGAATTACAGCGGAAATTACGGG	518
Qy	361	CATGCCAAAGGTCTGCTGGTATGGAACAGAACGAGGGGTTCTGGCTGATACACTCTGTT	420
Db	519	CATGCCAAAGGTCTGCTGGTATGGAACAGAGTGCAGGGGTTCTGGCTGATTCTATTCTATT	578
Qy	421	CCCAAGTTTCCCCCAGTTC-----ATGGCTATGAGTACCCAACCTCGGGGAGGCGATAT	474
Db	579	CCCAAGTTTCCCCCAGTTCCTCGGAAAAAGGCTATGAATACCCAAGCTCGGGGAGGCAATAT	638

Qy	1	ATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC	60
Db	40	ATGACAGCAAAGCCTCTAAGAACAGTTCTTTCTTTGCTCTTCTTTGCCCTCTCTGGGGTC	99
Qy	61	CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC	120
Db	100	CTGGGGACACCAGAAATCTCATGCAGAAATGAATATGGTGAAGCTGTGGACTGGTTTATC	159
Qy	121	TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG	180
Db	160	TTTTATAAGTTACCCAAAAGGACTAGCAAGGCAAGTGAAGAGGCGGGGCTGCAGTACCTG	219
Qy	181	TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAAACAGCACCAGG	240
Db	220	TACCTGGACTCCACAAGACAAACCTGGAACAAGAGCCTCTACCTGATTAAACAGCACCAGG	279
Qy	241	AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA	300
Db	280	AGTGCTCTGGGGAGGACCTTACAGCATCTGTATGACACACATAATTCCACGAATGACACA	339
Qy	301	GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA	360
Db	340	GCCTATCTAATATACAACGATGGTGTCCCTGGATCTGTGAATTACAGCAGACAGTATGGA	399
Qy	361	CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT	420
Db	400	CATGCCAAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTTCTGGCTGATACACTCTGTT	459
Qy	421	CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA	480
Db	460	CCCAAGTTTCCCCCAGTTCATGGCTATGAGTACCCAACCTCGGGGAGGCGATATGGACAA	519
Qy	481	ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG	540
Db	520	ACCGGCATCTGCATCACTTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG	579
Qy	541	GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	600
Db	580	GTCTTACAACCAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	639
Qy	601	TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	660
Db	640	TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	699
Qy	661	GAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	720
Db	700	GAACTGCACTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	759
Qy	721	GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC	780
Db	760	GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC	819
Qy	781	TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAAC	840
Db	820	TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAACCTGTTCCCTGCCTTACCATGTCTACAAC	879
Qy	841	ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA	900
Db	880	ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA	939
Qy	901	TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	960
Db	940	TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	999
Qy	961	AGCCTACACCAAGCCTTAAGAGGTGGAGGATTATCTGTACAAAGAATCACTACATTTAC	1020

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Db      1000 AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC 1059
Qy      1021 CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG 1062
        |||||||||||||||||||||||||||||||||||||||
Db      1060 CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG 1101

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Qy	541	GTCTTACAACCAAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	600
Db	580	GTCTTACAACCAAAACATCTACAGCTGCTTCATTCCAAGCACCTTTCACTGGAAACTTATC	639
Qy	601	TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	660
Db	640	TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	699
Qy	661	GAAGTGCCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	720
Db	700	GAAGTGCCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	759
Qy	721	GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC	780
Db	760	GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTTAGCACAAACC	819
Qy	781	TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	840
Db	820	TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	879
Qy	841	ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA	900
Db	880	ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA	939
Qy	901	TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	960
Db	940	TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	999
Qy	961	AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC	1020
Db	1000	AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC	1059
Qy	1021	CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG	1062
Db	1060	CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAAG	1101

Db	465	CTGATATACAATGACGCTGTCCCTGCATCTGTGAATTACAGCGGAAATTACGGGCATGCC	524
Qy	301	AAAGGTCTGCTGGTATGGAACAGAACGCAGGGGTCTGGCTGATACACTCTGTTCCCAAG	360
Db	525	AAAGGTCTGCTGGTATGGAACAGAGTGCAGGGGTCTGGCTGATTCACTTCTATTCCCAAG	584
Qy	361	TTTCCCCCAGTTC-----ATGGCTATGAGTACCCAACTCGGGGAGGCGATATGGACAA	414
Db	585	TTTCCCCCAGTTCGGGAAAAGGCTATGAATACCCAAAGCTCGGGGAGGCAATATGCACAA	644
Qy	415	ACCGGCATCTGCATCACTTTCGGATACAGCCAGTTTGAGGAAATAGATTTTCAGCTCTTG	474
Db	645	AGTGGCCTCTGCATCACTCTCAAATACAGCCAGTATGAGACAATAGATTCTCAGCTCTTG	704
Qy	475	GTCTTACAACCAACATCTACAGCTGCTTCATTCCAAGCACCTTTCAGTGGAACTTATC	534
Db	705	GTCTTCCAGCCAAACATCTACAGCTGTTTCATCCCAAACATCTTTCGCTGGGAACTCATC	764
Qy	535	TACATGCCCCGGATGTGTGCCAACTCCAGTTCCTTAAAGATCCCTGTCCGGTACCTCGCT	594
Db	765	CACATGCCTCAGATGTGTGCCAAGTCCAGTGCCTCAAAGATCCCTAGCCGGCGCCTCACT	824
Qy	595	GAAGTGCAGTCTCAGCCCAGGGTCTAAACTTCGTCCATTTTGCAAAATCAAGTTTTTATACT	654
Db	825	GTACTTCAGTCTCAGCCCAGGGTCTAAACTTCCTCCATTTTGCGAAATCAACTTTTTATACT	884
Qy	655	GATGACATCTTTACAGGATGGATAGCTCAAAAGTTGAAGACACATTTGTGTAGCACAAACC	714
Db	885	GATGACATCTTTGCAGCCTGGATAGCTCAAAAGCTGAAGGTGCATTTGTCTGGTAGAATCC	944
Qy	715	TGGCAGAAAAAGAAACAAGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	774
Db	945	TGGCAGCGAAAGAACCACGAGCTTCCTTCAAAGTGTTCCTGCCTTACCATGTCTACAAC	1004
Qy	775	ATCAAGTCCATTGGGGTAACTTCCAAGTCTTACTTCAGTTCTCGCCAAGACCATTCCAAA	834
Db	1005	ATCAAGGCCATTGGGGACCTCTGCAGTCCGACTTCCCTTCTCATCACGACCATTCCAAA	1064
Qy	835	TGGTGTGTTTCCATAAAGGGCTCCGCAAATCGCTGGACCTGCATTGGAGACCTAAATCGA	894
Db	1065	TGGTGTGTTTCCACAAAGGACTCTCAGGCTCGCTGGACCTGTATTGGAGACCTAAATCGG	1124
Qy	895	AGCCTACACCAAGCCTTAAGAGGTGGAGGATTCATCTGTACAAAGAATCACTACATTTAC	954
Db	1125	AGCCACATCAAGCCTTGAGAAGTGGAGGATTTATCTGTTTGAAGAATCGGTACATTTAC	1184
Qy	955	CAGGCATTTTCATAAATTATATCTCCGTTATGGGTTCTGTAA	995
Db	1185	CAGTCATTTGATAGGTTAGTTTCCCATTTATGCCTCCTGTAA	1225